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## RAW SEQUENCE LISTING

DATE: 05/01/2002

PATENT APPLICATION: US/10/060,765

TIME: 11:52:29

Input Set : N:\Crif3\RULE60\10060765.raw

Output Set: N:\CRF3\05012002\J060765.raw

**ENTERED**

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1 <110> APPLICANT: Itoh, Nobuyuki
2   Kavanaugh, W. Michael
3 <120> TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
4   PRODUCTS
5 <130> FILE REFERENCE: PP-16758.001/201130.408
6 <140> CURRENT APPLICATION NUMBER: 10/060,765
7 <141> CURRENT FILING DATE: 2002-01-29
9 <150> PRIOR APPLICATION NUMBER: US/09/715,805
10 <151> PRIOR FILING DATE: 2000-11-16
13 <160> NUMBER OF SEQ ID NOS: 17
14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 659
18 <212> TYPE: DNA
19 <213> ORGANISM: Mus musculus
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (14)...(646)
23 <400> SEQUENCE: 1
24   gagcgcagcc ctg atg gaa tgg atg aga tct aga gtt ggg acc ctg gga      49
25           Met Glu Trp Met Arg Ser Arg Val Gly Thr Leu Gly
26           1           5           10
27   ctg tgg gtc cga ctg ctg ctg gct gtc ttc ctg ctg ggg gtc tac caa      97
28   Leu Trp Val Arg Leu Leu Leu Ala Val Phe Leu Leu Gly Val Tyr Gln
29           15           20           25
30   gca tac ccc atc cct gac tcc agc ccc ctc ctc cag ttt ggg ggt caa      145
31   Ala Tyr Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
32           30           35           40
33   gtc cgg cag agg tac ctc tac aca gat gac gac caa gac act gaa gcc      193
34   Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Asp Gln Asp Thr Glu Ala
35           45           50           55           60
36   cac ctg gag atc agg gag gat gga aca gtg gta ggc gca gca cac cgc      241
37   His Leu Glu Ile Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg
38           65           70           75
39   agt cca gaa agt ctc ctg gag ctc aaa gcc ttg aag cca ggg gtc att      289
40   Ser Pro Glu Ser Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile
41           80           85           90
42   caa atc ctg ggt gtc aaa gcc tct agg ttt ctt tgc caa cag cca gat      337
43   Gln Ile Leu Gly Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp
44           95           100           105
45   gga gct ctc tat gga tcg cct cac ttt gat cct gag gcc tgc agc ttc      385
46   Gly Ala Leu Tyr Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe
47           110           115           120

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48   aga gaa ctg ctg ctg gag gac ggt tac aat gtg tac cag tct gaa gcc 433
49   Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
50   125                               130                               135                               140
51   cat ggc ctg ccc ctg cgt ctg cct cag aag gac tcc cca aac cag gat 481
52   His Gly Leu Pro Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp
53   145                               150                               155
54   gca aca tcc tgg gga cct gtg cgc ttc ctg ccc atg cca ggc ctg ctc 529
55   Ala Thr Ser Trp Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu
56   160                               165                               170
57   cac gag ccc caa gac caa gca gga ttc ctg ccc cca gag ccc cca gat 577
58   His Glu Pro Gln Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp
59   175                               180                               185
60   gtg ggc tcc tct gac ccc ctg agc atg gta gag cct tta cag ggc cga 625
61   Val Gly Ser Ser Asp Pro Leu Ser Met Val Glu Pro Leu Gln Gly Arg
62   190                               195                               200
63   agc ccc agc tat gcg tcc tga ctcttcctga atc 659
64   Ser Pro Ser Tyr Ala Ser *
65   205                               210
67 <210> SEQ ID NO: 2
68 <211> LENGTH: 210
69 <212> TYPE: PRT
70 <213> ORGANISM: Mus musculus
71 <400> SEQUENCE: 2
72   Met Glu Trp Met Arg Ser Arg Val Gly Thr Leu Gly Leu Trp Val Arg
73   1                               5                               10                               15
74   Leu Leu Leu Ala Val Phe Leu Leu Gly Val Tyr Gln Ala Tyr Pro Ile
75   20                               25                               30
76   Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg
77   35                               40                               45
78   Tyr Leu Tyr Thr Asp Asp Asp Gln Asp Thr Glu Ala His Leu Glu Ile
79   50                               55                               60
80   Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg Ser Pro Glu Ser
81   65                               70                               75                               80
82   Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly
83   85                               90                               95
84   Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp Gly Ala Leu Tyr
85   100                              105                              110
86   Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu
87   115                              120                              125
88   Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro
89   130                              135                              140
90   Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp Ala Thr Ser Trp
91   145                              150                              155                              160
92   Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu His Glu Pro Gln
93   165                              170                              175
94   Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp Val Gly Ser Ser
95   180                              185                              190
96   Asp Pro Leu Ser Met Val Glu Pro Leu Gln Gly Arg Ser Pro Ser Tyr
97   195                              200                              205

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98      Ala Ser
99      210
101 <210> SEQ ID NO: 3
102 <211> LENGTH: 643
103 <212> TYPE: DNA
104 <213> ORGANISM: Homo sapiens
105 <220> FEATURE:
106 <221> NAME/KEY: CDS
107 <222> LOCATION: (9)...(638)
108 <400> SEQUENCE: 3
109      agccattg atg gac tcg gac gag acc ggg ttc gag cac tca gga ctg tgg 50
110      Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp
111      1 5 10
112      gtt tct gtg ctg gct ggt ctt ctg ctg gga gcc tgc cag gca cac ccc 98
113      Val Ser Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro
114      15 20 25 30
115      atc cct gac tcc agt cct ctc ctg caa ttc ggg ggc caa gtc cgg cag 146
116      Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln
117      35 40 45
118      cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc cac ctg gag 194
119      Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu
120      50 55 60
121      atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag agc ccc gaa 242
122      Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu
123      65 70 75
124      agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att caa atc ttg 290
125      Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu
126      80 85 90
127      gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat ggg gcc ctg 338
128      Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu
129      95 100 105 110
130      tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc cgg gag ctg 386
131      Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu
132      115 120 125
133      ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc cac ggc ctc 434
134      Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu
135      130 135 140
136      ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac cct gca ccc 482
137      Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro
138      145 150 155
139      cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc ccc gca ctc 530
140      Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Leu
141      160 165 170
142      ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat gtg ggc tcc 578
143      Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser
144      175 180 185 190
145      tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga agc ccc agc 626
146      Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser
147      195 200 205

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148      tac gct tcc tga agcca                                     643
149      Tyr Ala Ser  *
151 <210> SEQ ID NO: 4
152 <211> LENGTH: 209
153 <212> TYPE: PRT
154 <213> ORGANISM: Homo sapiens
155 <400> SEQUENCE: 4
156      Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser
157      1              5              10              15
158      Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
159      20              25              30
160      Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
161      35              40              45
162      Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
163      50              55              60
164      Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
165      65              70              75              80
166      Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
167      85              90              95
168      Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
169      100             105             110
170      Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
171      115             120             125
172      Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
173      130             135             140
174      His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
175      145             150             155             160
176      Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Leu Pro Glu
177      165             170             175
178      Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
179      180             185             190
180      Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala
181      195             200             205
182      Ser
184 <210> SEQ ID NO: 5
185 <211> LENGTH: 20
186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: PCR primer
190 <400> SEQUENCE: 5
191      agccattgat ggactcggac                                     20
193 <210> SEQ ID NO: 6
194 <211> LENGTH: 20
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: PCR primer
199 <400> SEQUENCE: 6

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Input Set : N:\Crf3\RULE60\10060765.raw

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```

200      tggcttcagg aagcgtagct
202 <210> SEQ ID NO: 7
203 <211> LENGTH: 16
204 <212> TYPE: PRT
205 <213> ORGANISM: Homo sapiens
206 <400> SEQUENCE: 7
207      Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His
208      1          5          10          15
210 <210> SEQ ID NO: 8
211 <211> LENGTH: 15
212 <212> TYPE: PRT
213 <213> ORGANISM: Homo sapiens
214 <400> SEQUENCE: 8
215      His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg
216      1          5          10          15
218 <210> SEQ ID NO: 9
219 <211> LENGTH: 218
220 <212> TYPE: PRT
221 <213> ORGANISM: Mus musculus
222 <400> SEQUENCE: 9
223      Met Ala Arg Lys Trp Asn Gly Arg Ala Val Ala Arg Ala Leu Val Leu
224      1          5          10          15
225      Ala Thr Leu Trp Leu Ala Val Ser Gly Arg Pro Leu Ala Gln Gln Ser
226      20          25          30
227      Gln Ser Val Ser Asp Glu Asp Pro Leu Phe Leu Tyr Gly Trp Gly Lys
228      35          40          45
229      Ile Thr Arg Leu Gln Tyr Leu Tyr Ser Ala Gly Pro Tyr Val Ser Asn
230      50          55          60
231      Cys Phe Leu Arg Ile Arg Ser Asp Gly Ser Val Asp Cys Glu Glu Asp
232      65          70          75          80
233      Gln Asn Glu Arg Asn Leu Leu Glu Phe Arg Ala Val Ala Leu Lys Thr
234      85          90          95
235      Ile Ala Ile Lys Asp Val Ser Ser Val Arg Tyr Leu Cys Met Ser Ala
236      100         105         110
237      Asp Gly Lys Ile Tyr Gly Leu Ile Arg Tyr Ser Glu Glu Asp Cys Thr
238      115         120         125
239      Phe Arg Glu Glu Met Asp Cys Leu Gly Tyr Asn Gln Tyr Arg Ser Met
240      130         135         140
241      Lys His His Leu His Ile Ile Phe Ile Gln Ala Lys Pro Arg Glu Gln
242      145         150         155         160
243      Leu Gln Asp Gln Lys Pro Ser Asn Phe Ile Pro Val Phe His Arg Ser
244      165         170         175
245      Phe Phe Glu Thr Gly Asp Gln Leu Arg Ser Lys Met Phe Ser Leu Pro
246      180         185         190
247      Leu Glu Ser Asp Ser Met Asp Pro Phe Arg Met Val Glu Asp Val Asp
248      195         200         205
249      His Leu Val Lys Ser Pro Ser Phe Gln Lys
250      210         215
252 <210> SEQ ID NO: 10

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VERIFICATION SUMMARY

DATE: 05/01/2002

PATENT APPLICATION: US/10/060,765

TIME: 11:52:30

Input Set : N:\Crf3\RULE60\10060765.raw

Output Set: N:\CRF3\05012002\J060765.raw